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Drome-CLK      -----GMEKVDANAYELVKFVGYFR-----NDTNTSTGSSSEV
Tal-CLK        -----QQHQQQQPQQHQ
Macro-CLK      -----SVSSCSRSMFGGNAG-----GGVTGSSNAGSGL
Ep-CLK         PEEYRERYTIAIHIQRGGMTPTAVPVYERIHLTGYFERYKCPSEDGVLDVDFSCSEAEDSSM
                . .

Drome-CLK      SNGSNGQPAVLPRIFQQNPNAEVDKLVFVGTGRVQNPQLIREMSIIDPTSNEFTSKHSM
Tal-CLK        QPQHPPQRPQEQQQQLQRNDQPEQNQPVFVVGICRLEQPQLLREMRLLERTNTEFVSRHSL
Macro-CLK      CQSS-----LVQTNPSQEP-TKLVFVAIGRLERPQLVREMMIIEPSKTEFTSRHSL
Ep-CLK         SVGGTSRSSNPSPFTHSQHHSPEPTKIVFVAIARLEHPQLLRELIVLEPTKSEFTSRHSL
                . . . . .
                .: ***. *:::***:***: ::: :..**.*:***:

Drome-CLK      EWKFLFLDHRAPPIIGYMPFEVLGTSGYDYYHFDDLDSIVACHEELRQTGEGKSCYYRFL
Tal-CLK        EWKFLFLDQRASAIIGYLPFEVLGTSGYDYYHVDDLERVSTCHQFLIRTGKGS SCYYRFL
Macro-CLK      EWKFLFLDHRAPTIIGYLPFEVLGTSGYDYYHVEDLDKVASCHEQLMKTGKGTSCYYRFL
Ep-CLK         EWKFLFLDHRAPTIIGYLPFEVLGTSGYDYYHVDDLKLVSECHEMLMKKKGKISCFYRFL
                *****:*. .***:*****:*****:***: : **:* .:* **:*

Drome-CLK      TKGQQWIWLQTDYVVSYHQFNPKPDYVCTHKVVSYAEVLKDSRKEGQKSGNSNSITNNG
Tal-CLK        TKGHQVWVWLQSHYYISYHQWNSKPEFVCTNTVVSYDDIKAEKLNSSSTNYNDSSTNLQTS
Macro-CLK      TKGQQWIWLQTYIITYHQWNSKPEFVCTNTVVSYS DVKAEKLVKEQMPNGLSELEINQS
Ep-CLK         TKGQQWIWLRSHYCITYHQWNSKPEFVCTNTVVSYGNIKGNNQQNHSEEREKSDMEFES
                ***:***:***:.* :*:***:***:***:***:***: : : . . .

Drome-CLK      SSKVIASTGTSSKSA-----
Tal-CLK        SLTEDKTVSSSCPSQNCTFAEKIDPETKCKSEQNQRRFFQKIQSFEEQCMNSSSRAEQSSS
Macro-CLK      ES----SMGLSGAGP-----
Ep-CLK         HSQP-TSEGGGSFAP-----
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Figure S4. Putative *Talitrus saltator* CLOCK (CLK) protein

Alignment of *Drosophila melanogaster* CLK (Drome-CLK; Accession No. AAC62234) with the *T. saltator* CLK (Tal-CLK) deduced from the Trinity *de novo* transcriptome assembly, together with the top two tblastn species homologue sequences *Macrobrachium rosenbergii* CLK (Macro-CLK; Accession No. AY842303) and *Eurydice pulchra* CLK (Ep-CLK; Accession No. KC885976). 3' sequence removed from all sequences. 5' sequence removed from all sequences except Tal-CLK to aid alignment. '*' indicates identical amino acid residues in the two proteins, '.' and ':' indicate similar amino acid residues between the two proteins. In this figure SMART identified domains consisting of one PAS domain and one PAC domain are highlighted in green and blue respectively.